

## SEQUENCE LISTING

<110> Presnell, Scott R.  
 Xu, Wenfeng  
 Novak, Julia E.  
 Whitmore, Theodore E.  
 Grant, Francis J.

<120> CYTOKINE RECEPTOR ZCYTOR19

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<150> US 60/253,561

<151> 2000-11-28

<150> US 60/267,211

<151> 2001-02-07

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<211> 1476

<212> DNA

<213> Homo sapiens

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<221> CDS

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Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu	
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ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc	144

0995898-11201

Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly	
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Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr	
50 55 60	
cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg	240
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu	
65 70 75 80	
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc	288
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe	
85 90 95	
aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg	336
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val	
100 105 110	
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct	384
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro	
115 120 125	
gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg	432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr	
130 135 140	
tac cag ctg ccc ccc tgc atg ccc cca ctg ttt ctg aag tat gag gtg	480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val	
145 150 155 160	
gca ttt tgg ggg ggg ggg gcc gga acc aag acc cta ttt cca gtc act	528
Ala Phe Trp Gly Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr	
165 170 175	
ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa	576
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu	
180 185 190	
cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa	624
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys	
195 200 205	

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Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu	
210 215 220	
gcc aac tgg gct ttc ctg gtg ctg cca tcg ctt ctg ata ctg ctg tta	720
Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu	
225 230 235 240	
gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc	768
Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro	
245 250 255	
tgg ttt cag cgg gca aag atg cca cgg gcc ctg gaa ctg acc aga ggg	816
Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly	
260 265 270	
gtc agg ccg acg cct cga gtc agg gcc cca gcc acc caa cag aca aga	864
Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg	
275 280 285	
tgg aag aag gac ctt gca gag gac gaa gag gag gag gat gag gag gac	912
Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp	
290 295 300	
aca gaa gat ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc	960
Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe	
305 310 315 320	
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Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val	
325 330 335	
gac tca ggg agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct	1056
Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser	
340 345 350	
gct tgg gat tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc	1104
Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser	
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tgg gac agg gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc	1152
Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly	
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ttc tcc aag gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc 1248  
 Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu  
 405 410 415

tcc tcc tgg gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc 1296  
 Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val  
 420 425 430

cct ggg gga ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa 1344  
 Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu  
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agc agc cct gag gag gaa gag gag gcg agg gaa tca gaa att gag gac 1392  
 Ser Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp  
 450 455 460

agc gat gcg ggc agc tgg ggg gct gag agc acc cag agg acc gag gac 1440  
 Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp  
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agg ggc cgg aca ttg ggg cat tac atg gcc agg tga 1476  
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<211> 491

<212> PRT

<213> Homo sapiens

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 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly  
 35 40 45

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Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu
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Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe
				85					90					95	
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val
			100					105					110		
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro
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Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr
		130				135					140				
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Phe	Leu	Lys	Tyr	Glu	Val
145					150					155					160
Ala	Phe	Trp	Gly	Gly	Gly	Ala	Gly	Thr	Lys	Thr	Leu	Phe	Pro	Val	Thr
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Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu
			180					185					190		
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		195					200					205			
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu
		210				215					220				
Ala	Asn	Trp	Ala	Phe	Leu	Val	Leu	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu
225					230					235					240
Val	Ile	Ala	Ala	Gly	Gly	Val	Ile	Trp	Lys	Thr	Leu	Met	Gly	Asn	Pro
			245						250					255	
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			260					265					270		
Val	Arg	Pro	Thr	Pro	Arg	Val	Arg	Ala	Pro	Ala	Thr	Gln	Gln	Thr	Arg
		275					280					285			
Trp	Lys	Lys	Asp	Leu	Ala	Glu	Asp	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Asp
		290				295				300					
Thr	Glu	Asp	Gly	Val	Ser	Phe	Gln	Pro	Tyr	Ile	Glu	Pro	Pro	Ser	Phe
305					310					315					320
Leu	Gly	Gln	Glu	His	Gln	Ala	Pro	Gly	His	Ser	Glu	Ala	Gly	Gly	Val
			325						330					335	
Asp	Ser	Gly	Arg	Pro	Arg	Ala	Pro	Leu	Val	Pro	Ser	Glu	Gly	Ser	Ser
			340					345				350			
Ala	Trp	Asp	Ser	Ser	Asp	Arg	Ser	Trp	Ala	Ser	Thr	Val	Asp	Ser	Ser
		355					360					365			
Trp	Asp	Arg	Ala	Gly	Ser	Ser	Gly	Tyr	Leu	Ala	Glu	Lys	Gly	Pro	Gly
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Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu  
 385 390 395 400  
 Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu  
 405 410 415  
 Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val  
 420 425 430  
 Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu  
 435 440 445  
 Ser Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp  
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<212> DNA

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ytnacntggy tncnggny tngnaayccn caryaygt na tntaytygt ngcntaycar	180
wsnwsnccna cnmgnmgng ntggmgngar gtngargart gygcnggnac naargarytn	240
ytnygywsna tgatgtgyt naaraarcar gayytnaya ayaarttyaa rggngmgngtn	300
mgncngtnw sncnwsnws naarwsnccn tgggtngarw sngartayt ngaytaytn	360
ttygargtng arcngcnc nccngtnytn gtnytnacnc aracngarga rathytnwsn	420
gcnaaygcna cntaycaryt nccncntgy atgcncncny tnttyytnaa rtaygargtn	480
gcnttytggg gngngnggc nggnacnaar acnytnntyc cngtnacncc ncayggncar	540
ccngtncara thacnytnca rccngcngcn wsnargcayc aytgyytnws ngcnmgngn	600
athtayacnt tywsngtncc naartaywsn aarttywsna arccnacntg ytttytnytn	660
gargtnccng argcnaaytg ggcnttytn gtnytnccnw snytnytnat hytnytnytn	720
gtnathgcng cngngngngt nathtggaar acnytnatgg gnaayccntg gttycarmgn	780
gcnaaratgc cnmngncny ngarytnacn mgngnggtm gncnacncc nmngngtnmgn	840
gcncngcna cncarcarac nmngtggaar aargayytn cngargayga rgargargar	900

gaygargarg ayacngarga yggngtnwsn tttycarccnt ayathgarcc nccnwsntty 960  
 ytnggncarg arcaycargc nccnggncay wsnrgargcng gngngngtnga ywsnggnmgn 1020  
 ccnmgngcnc cnytngtnc nwsngarggn wsnwsngcnt gggaywsnws ngaymgnwsn 1080  
 tgggcnwsna cngtngayws nwsntgggay mgngcnggnw snwsnggnta yytngcngar 1140  
 aarggncng gncarggnc ngngngngay ggncaycarg arwsnytncc nccnccngar 1200  
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 acntgggna cnytnccncc ngarccnaay ytngtnccng gnggncncc ngtnwsnytn 1320  
 caracnytna cnttytytg ggarwsnwsn ccngargarg argargargc nmngngarwsn 1380  
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 Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr Arg Arg Arg Trp  
 35 40 45  
 Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu Leu Cys Ser Met  
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 Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe Lys Gly Arg Val  
 65 70 75 80  
 Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val Glu Ser Glu Tyr  
 85 90 95  
 Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro Val Leu Val Leu  
 100 105 110  
 Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr Tyr Gln Leu Pro  
 115 120 125  
 Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val Ala Phe Trp Gly  
 130 135 140  
 Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr Pro His Gly Gln  
 145 150 155 160  
 Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu His His Cys Leu  
 165 170 175  
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 Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro  
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TOGETT "888588660

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 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180  
 aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 240  
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 ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc 360  
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 cccgtgctgg actccgacgg ctcttcttc ctctacagca agctcaccgt ggacaagagc 600  
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agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac	96
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr	
20 25 30	
ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc	144
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser	
35 40 45	
ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc	192
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser	
50 55 60	
ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc	240
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr	
65 70 75 80	
tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag	288
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys	
85 90 95	
aaa gtt gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc	336
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys	
100 105 110	
cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca	384
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro	
115 120 125	
aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc	432
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys	
130 135 140	
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Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp	
145 150 155 160	
tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag	528
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu	
165 170 175	
gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg	576
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu	
180 185 190	

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cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac	624
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn	
195 200 205	
aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg	672
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly	
210 215 220	
cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag	720
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu	
225 230 235 240	
ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat	768
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr	
245 250 255	
ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac	816
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn	
260 265 270	
aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc	864
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe	
275 280 285	
ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac	912
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn	
290 295 300	
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Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr	
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Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
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&lt;211&gt; 330

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

T082T"885660

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 35 40 45  
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 50 55 60  
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 65 70 75 80  
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 85 90 95  
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
 100 105 110  
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
 115 120 125  
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
 130 135 140  
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
 145 150 155 160  
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
 165 170 175  
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
 180 185 190  
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
 195 200 205  
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
 210 215 220  
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu  
 225 230 235 240  
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
 245 250 255  
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
 260 265 270  
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
 275 280 285  
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
 290 295 300  
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
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Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln	
1 5 10 15	
ttg aaa tct ggt acc gcc tct gtt gtg tgc ctg ctg aat aac ttc tat	96
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr	
20 25 30	
ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg	144
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser	
35 40 45	
ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc	192
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr	
50 55 60	
tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa	240
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys	
65 70 75 80	
cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc	288
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro	
85 90 95	
gtc aca aag agc ttc aac agg gga gag tgt tag	321
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *	
100 105	

<210> 17  
 <211> 106  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

```

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1          5          10          15
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
          20          25          30
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
          35          40          45
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
          50          55          60
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65          70          75          80
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
          85          90          95
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
          100          105

```

&lt;210&gt; 18

&lt;211&gt; 1563

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1563)

&lt;400&gt; 18

```

atg gcg ggg ccc gag cgc tgg ggc ccc ctg ctc ctg tgc ctg ctg cag      48
Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1          5          10          15

gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg      96
Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
          20          25          30

ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc      144
Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
          35          40          45

aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc      192
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
          50          55          60

```

cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg	240
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu	
65 70 75 80	
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc	288
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe	
85 90 95	
aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg	336
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val	
100 105 110	
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct	384
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro	
115 120 125	
gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg	432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr	
130 135 140	
tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg	480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val	
145 150 155 160	
gca ttc tgg aag gag ggg gcc gga aac aag acc cta ttt cca gtc act	528
Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr	
165 170 175	
ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa	576
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu	
180 185 190	
cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa	624
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys	
195 200 205	
tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa	672
Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu	
210 215 220	
gcc aac tgg gct ttc ctg gtg ctg cca tcg ctt ctg ata ctg ctg tta	720



Ala 225	Asn	Trp	Ala	Phe	Leu 230	Val	Leu	Pro	Ser	Leu 235	Leu	Ile	Leu	Leu	Leu 240		
gta	att	gcc	gca	ggg	ggt	gtg	atc	tgg	aag	acc	ctc	atg	ggg	aac	ccc	768	
Val	Ile	Ala	Ala	Gly 245	Gly	Val	Ile	Trp	Lys 250	Thr	Leu	Met	Gly	Asn 255	Pro		
tgg	ttt	cag	cgg	gca	aag	atg	cca	cgg	gcc	ctg	gac	ttt	tct	gga	cac	816	
Trp	Phe	Gln	Arg 260	Ala	Lys	Met	Pro	Arg	Ala 265	Leu	Asp	Phe	Ser	Gly	His		
aca	cac	cct	gtg	gca	acc	ttt	cag	ccc	agc	aga	cca	gag	tcc	gtg	aat	864	
Thr	His	Pro 275	Val	Ala	Thr	Phe	Gln 280	Pro	Ser	Arg	Pro	Glu 285	Ser	Val	Asn		
gac	ttg	ttc	ctc	tgt	ccc	caa	aag	gaa	ctg	acc	aga	ggg	gtc	agg	ccg	912	
Asp	Leu 290	Phe	Leu	Cys	Pro	Gln 295	Lys	Glu	Leu	Thr	Arg 300	Gly	Val	Arg	Pro		
acg	cct	cga	gtc	agg	gcc	cca	gcc	acc	caa	cag	aca	aga	tgg	aag	aag	960	
Thr 305	Pro	Arg	Val	Arg 310	Ala	Pro	Ala	Thr	Gln	Gln 315	Thr	Arg	Trp	Lys	Lys 320		
gac	ctt	gca	gag	gac	gaa	gag	gag	gag	gat	gag	gag	gac	aca	gaa	gat	1008	
Asp	Leu	Ala	Glu	Asp 325	Glu	Glu	Glu	Glu	Asp 330	Glu	Glu	Asp	Thr	Glu	Asp 335		
ggc	gtc	agc	ttc	cag	ccc	tac	att	gaa	cca	cct	tct	ttc	ctg	ggg	caa	1056	
Gly	Val	Ser 340	Phe	Gln	Pro	Tyr	Ile	Glu	Pro	Pro	Ser	Phe	Leu	Gly	Gln		
gag	cac	cag	gct	cca	ggg	cac	tcg	gag	gct	ggt	ggg	gtg	gac	tca	ggg	1104	
Glu	His 355	Gln	Ala	Pro	Gly	His	Ser 360	Glu	Ala	Gly	Gly	Val	Asp	Ser	Gly		
agg	ccc	agg	gct	cct	ctg	gtc	cca	agc	gaa	ggc	tcc	tct	gct	tgg	gat	1152	
Arg 370	Pro	Arg	Ala	Pro	Leu	Val 375	Pro	Ser	Glu	Gly	Ser 380	Ser	Ala	Trp	Asp		
tct	tca	gac	aga	agc	tgg	gcc	agc	act	gtg	gac	tcc	tcc	tgg	gac	agg	1200	
Ser 385	Ser	Asp	Arg	Ser 390	Trp	Ala	Ser	Thr	Val	Asp 395	Ser	Ser	Trp	Asp	Arg 400		

gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc caa ggg ccg 1248  
 Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro  
 405 410 415

ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa ttc tcc aag 1296  
 Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys  
 420 425 430

gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc tcc tcc tgg 1344  
 Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp  
 435 440 445

gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc cct ggg gga 1392  
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly  
 450 455 460

ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa agc agc cct 1440  
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro  
 465 470 475 480

gag gag gaa gag gag gcg agg gaa tca gaa att gag gac agc gat gcg 1488  
 Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala  
 485 490 495

ggc agc tgg ggg gct gag agc acc cag agg acc gag gac agg ggc cgg 1536  
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg  
 500 505 510

aca ttg ggg cat tac atg gcc agg tga 1563  
 Thr Leu Gly His Tyr Met Ala Arg \*

&lt;210&gt; 19

&lt;211&gt; 520

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln  
 1 5 10 15  
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu  
 20 25 30

0995898-12801

Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly  
 35 40 45  
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr  
 50 55 60  
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu  
 65 70 75 80  
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe  
 85 90 95  
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val  
 100 105 110  
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro  
 115 120 125  
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr  
 130 135 140  
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val  
 145 150 155 160  
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr  
 165 170 175  
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu  
 180 185 190  
 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys  
 195 200 205  
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu  
 210 215 220  
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu  
 225 230 235 240  
 Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro  
 245 250 255  
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His  
 260 265 270  
 Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn  
 275 280 285  
 Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro  
 290 295 300  
 Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys  
 305 310 315 320  
 Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp  
 325 330 335  
 Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln  
 340 345 350  
 Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly  
 355 360 365

0095898.12801  
 T0821T. B585660

Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp  
 370 375 380  
 Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg  
 385 390 395 400  
 Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro  
 405 410 415  
 Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys  
 420 425 430  
 Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp  
 435 440 445  
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly  
 450 455 460  
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro  
 465 470 475 480  
 Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala  
 485 490 495  
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg  
 500 505 510  
 Thr Leu Gly His Tyr Met Ala Arg  
 515 520

<210> 20  
 <211> 674  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(633)

<400> 20

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 1 5 10 15

gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96  
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu  
 20 25 30

ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144  
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly  
 35 40 45

0995698-112801

aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc 192  
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr  
 50 55 60

cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg 240  
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu  
 65 70 75 80

cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc 288  
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe  
 85 90 95

aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg 336  
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val  
 100 105 110

gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct 384  
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro  
 115 120 125

gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg 432  
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr  
 130 135 140

tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg 480  
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val  
 145 150 155 160

gca ttc tgg aag gag ggg gcc gga aac aag gtg gga agc tcc ttt cct 528  
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro  
 165 170 175

gcc ccc agg cta ggc ccg ctc ctc cac ccc ttc tta ctc agg ttc ttc 576  
 Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe  
 180 185 190

tca ccc tcc cag cct gct cct gca ccc ctc ctc cag gaa gtc ttc cct 624  
 Ser Pro Ser Gln Pro Ala Pro Ala Pro Leu Leu Gln Glu Val Phe Pro  
 195 200 205

gta cac tcc tgacttctgg cagtcagccc taataaaaatc tgatcaaaagt 673  
 Val His Ser  
 210

099558-12004

674

[illegible]

<210> 22  
<211> 1422  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Zcytor17-Fc4 fusion protein

&lt;221&gt; CDS

&lt;222&gt; (1)...(1422)

&lt;400&gt; 22

atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt ggc	48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly	
1 5 10 15	
gcc gtc ttc gtt tgc ctc agc cag gaa atc cat gcc gag ttg aga cgc	96
Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg	
20 25 30	
ttc cgt aga tcc agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg	144
Phe Arg Arg Ser Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu	
35 40 45	
ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc	192
Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly	
50 55 60	
aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc	240
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr	
65 70 75 80	
cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg	288
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu	
85 90 95	
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc	336
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe	
100 105 110	
aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg	384
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val	
115 120 125	
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct	432
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro	
130 135 140	

F082T" 868660

gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr 145 150 155 160	480
tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val 165 170 175	528
gca ttc tgg aag gag ggg gcc gga aac aag acc cta ttt cca gtc act Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr 180 185 190	576
ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu 195 200 205	624
cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys 210 215 220	672
tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu 225 230 235 240	720
gcc aac tgg aga tct tca gac aaa act cac aca tgc cca ccg tgc cca Ala Asn Trp Arg Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro 245 250 255	768
gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc ccc cca aaa Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys 260 265 270	816
ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val 275 280 285	864
gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr 290 295 300	912
gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu 305 310 315 320	960



cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac	1008
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His	
325 330 335	
cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa	1056
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys	
340 345 350	
gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc aaa ggg cag	1104
Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln	
355 360 365	
ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg	1152
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu	
370 375 380	
acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc	1200
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro	
385 390 395 400	
agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac	1248
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn	
405 410 415	
tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc	1296
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu	
420 425 430	
tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc	1344
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val	
435 440 445	
ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag	1392
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln	
450 455 460	
aag agc ctc tcc ctg tct ccg ggt aaa taa	1422
Lys Ser Leu Ser Leu Ser Pro Gly Lys *	
465 470	

&lt;211&gt; 473

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;400&gt; 23

Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Val	Leu	Leu	Leu	Cys	Gly
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Ala	Val	Phe	Val	Ser	Leu	Ser	Gln	Glu	Ile	His	Ala	Glu	Leu	Arg	Arg
			20					25					30		
Phe	Arg	Arg	Ser	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu
			35				40					45			
Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly
	50					55					60				
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr
65					70					75					80
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu
				85					90					95	
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe
			100					105					110		
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val
		115					120						125		
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro
		130				135					140				
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr
145					150					155					160
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val
				165					170					175	
Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Thr	Leu	Phe	Pro	Val	Thr
			180					185					190		
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu
		195					200					205			
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys
	210					215					220				
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu
225					230					235				240	
Ala	Asn	Trp	Arg	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
				245					250					255	
Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
		260					265						270		
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
		275					280					285			
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr
	290					295					300				

F08211" 86856660

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
 305 310 315 320  
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
 325 330 335  
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
 340 345 350  
 Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
 355 360 365  
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
 370 375 380  
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
 385 390 395 400  
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
 405 410 415  
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
 420 425 430  
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
 435 440 445  
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
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 Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 465 470

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28

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<212> DNA

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<223> Oligonucleotide primer ZC37685

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<223> Oligonucleotide primer ZC37681

<400> 27

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22

<210> 28

<211> 1560

<212> DNA

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N0:19

<221> misc\_feature

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<223> n = A,T,C or G

<400> 28

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mgncnmgny tngcncncc ncaraaygt nacytnytnw snaraaytt ywsngntay	120
ytnacntggy tncnggny nggnaayccn cargaygt na cntayttygt ngcntaycar	180
wsnwsnccna cnmgngmg ngtgmgngar gtngargart gygcnggnac naargarytn	240
ytntgywsna tgatgtgyyt naaraarcar gayytnaya ayaarttyaa rggngmgntn	300

mgnacngtnw	sncnwsnws	naarwsnccn	tgggtngarw	sngartayyt	ngaytayytn	360
ttygargtn	arccngcncc	nccngtnytn	gtnytnacnc	aracngarga	rathytnwsn	420
gcnaaygcna	cntaycaryt	nccncntgy	atgccnccny	tngayytnaa	rtaygargtn	480
gcnttytgga	argarggngc	nggnaayaar	acnytnnttyc	cngtnacncc	ncayggncar	540
ccngtncara	thacnytnca	rccngcngcn	wsngarcayc	aytgyytnws	ngcnmgnacn	600
athtayacnt	tywsngtncc	naartaywsn	aarttywsna	arccnacntg	ytyytnytn	660
gargtnccng	argcnaaytg	ggcnttyytn	gtnytnccnw	snytnytnat	hytnytnytn	720
gtnathgcng	cngggngngt	nathtggaar	acnytnatgg	gnaayccntg	gttycarmgn	780
gcnaaratgc	cnmngncny	ngayttywsn	ggncayaacnc	ayccngtngc	nacnttycar	840
ccnwsnmgnc	cngarwsngt	naaygayytn	ttyytnntgy	cncaraarga	rytnacnmgn	900
ggngtnmgnc	cnacnccnmg	ngtnmgngcn	ccngcnacnc	arcaracnmg	ntggaaraar	960
gayytnngcng	argaygarga	rgargargay	gargargaya	cngargaygg	ngtnwsntty	1020
carccntaya	thgarccncc	nwsnttyytn	ggncargarc	aycargcncc	nggncaywsn	1080
gargcnggng	gngtngayws	nggnmgncn	mgngcnccny	tngtnccnws	ngarggnwsn	1140
wsngcntggg	aywsnwsnga	ymgnwsntgg	gcnwsnacng	tngaywsnws	ntgggaymgn	1200
gcnggnwsnw	snggntayyt	ngcngaraar	ggncnccngc	arggncnccng	nggngayggn	1260
caycargarw	snytnccncc	nccngartty	wsnaargayw	snggnttyyt	ngargarytn	1320
ccngargaya	ayytnwsnws	ntgggcnacn	tggggnacny	tccnccnga	rccnaayytn	1380
gtncnccngng	gncnccngt	nwsnytnear	acnytnacnt	tytgytgga	rwsnwsnccn	1440
gargargarg	argargcnmg	ngarwsngar	athgargayw	sngaygcngg	nwsntggggn	1500
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<211> 633

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ytnacntggy	tncnccngny	nggnaayccn	cargaygt	cntayttygt	ngcntaycar	180
wsnwsnccna	cnmgnmgng	ntggmgngar	gtngargart	gygcnggnac	naargarytn	240
ytnygywsna	tgatgtgyyt	naaraarcar	gayytnntaya	ayaarttyaa	rggnmgngtn	300
mgnacngtnw	sncnwsnws	naarwsnccn	tgggtngarw	sngartayyt	ngaytayytn	360
ttygargtn	arccngcncc	nccngtnytn	gtnytnacnc	aracngarga	rathytnwsn	420
gcnaaygcna	cntaycaryt	nccncntgy	atgccnccny	tngayytnaa	rtaygargtn	480

gcnttytgga argarggngc nggnaayaar gtnggnwsnw snttyccngc nccnmgnytn 540  
 ggncnytny tncayccntt yytnytnmgn ttyttywsnc cnwsncarcc ngcncngcn 600  
 ccnytnytn argargtntt yccngtncay wsn 633

<210> 30

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Primer ZC39204

<400> 30

tcaccacgcg aattcggtag cgctggttcc gcgtggatcc aggccccgtc tggccccctcc 60  
 ccag 64

<210> 31

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Primer ZC39205

<400> 31

tctgtatcag gctgaaaatc ttatctcatc cgccaaaaca ccagttggct tctgggacct 60  
 ccag 64

<210> 32

<211> 1922

<212> DNA

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<220>

<223> MBP-human zcytoR19 fusion protein polynucleotide  
 sequence

<221> CDS

<222> (123)...(1922)

<400> 32

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 caggaaacag ccagtccgtt taggtgtttt cacgagcact tcaccaacaa ggaccataga 120

tt atg aaa act gaa gaa ggt aaa ctg gta atc tgg att aac ggc gat	167
Met Lys Thr Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp	
1 5 10 15	
aaa ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat	215
Lys Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp	
20 25 30	
acc gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa	263
Thr Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys	
35 40 45	
ttc cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg	311
Phe Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp	
50 55 60	
gca cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa	359
Ala His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu	
65 70 75	
atc acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg	407
Ile Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp	
80 85 90 95	
gat gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt	455
Asp Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val	
100 105 110	
gaa gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca	503
Glu Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro	
115 120 125	
aaa acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa	551
Lys Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys	
130 135 140	
ggt aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg	599
Gly Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp	
145 150 155	
ccg ctg att gct gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc	647
Pro Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly	
160 165 170 175	

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aag tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg	695
Lys Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala	
180 185 190	
ggt ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca	743
Gly Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala	
195 200 205	
gac acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca	791
Asp Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr	
210 215 220	
gcg atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc	839
Ala Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser	
225 230 235	
aaa gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca	887
Lys Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro	
240 245 250 255	
tcc aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt	935
Ser Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser	
260 265 270	
ccg aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act	983
Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr	
275 280 285	
gat gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta	1031
Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val	
290 295 300	
gcg ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc	1079
Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala	
305 310 315	
gcc acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg	1127
Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro	
320 325 330 335	
cag atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc	1175



Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala	
340 345 350	
gcc agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act	1223
Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr	
355 360 365	
aat tcg agc tcc cac cat cac cat cac gcc aat tcg gta ccg ctg	1271
Asn Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu	
370 375 380	
gtt ccg cgt gga tcc agg ccc cgt ctg gcc cct ccc cag aat gtg acg	1319
Val Pro Arg Gly Ser Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr	
385 390 395	
ctg ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt	1367
Leu Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu	
400 405 410 415	
ggc aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc	1415
Gly Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro	
420 425 430	
acc cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag	1463
Thr Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu	
435 440 445	
ctg cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag	1511
Leu Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys	
450 455 460	
ttc aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg	1559
Phe Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp	
465 470 475	
gtg gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca	1607
Val Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro	
480 485 490 495	
cct gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc	1655
Pro Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala	
500 505 510	

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acg tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag 1703  
 Thr Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu  
                   515                                  520                                  525

gtg gca ttc tgg aag gag ggg gcc gga aac aag acc cta ttt cca gtc 1751  
 Val Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val  
                   530                                  535                                  540

act ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc 1799  
 Thr Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser  
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gaa cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg 1847  
 Glu His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro  
 560                                  565                                  570                                  575

aaa tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca 1895  
 Lys Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro  
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gaa gcc aac tgg tgt ttt ggc gga tga 1922  
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 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr  
                   20                                  25                                  30  
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe  
                   35                                  40                                  45  
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala  
                   50                                  55                                  60

0595898-11201

His	Asp	Arg	Phe	Gly	Gly	Tyr	Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	
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Thr	Pro	Asp	Lys	Ala	Phe	Gln	Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	
				85					90					95		
Ala	Val	Arg	Tyr	Asn	Gly	Lys	Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	
				100				105					110			
Ala	Leu	Ser	Leu	Ile	Tyr	Asn	Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	
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Thr	Trp	Glu	Glu	Ile	Pro	Ala	Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	
	130					135					140					
Lys	Ser	Ala	Leu	Met	Phe	Asn	Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	
145					150					155					160	
Leu	Ile	Ala	Ala	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys	
				165					170					175		
Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly	
			180					185					190			
Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp	
		195				200						205				
Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala	
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Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	
225					230					235					240	
Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser	
			245						250					255		
Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro	
			260					265					270			
Asn	Lys	Glu	Leu	Ala	Lys	Glu	Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp	
		275					280					285				
Glu	Gly	Leu	Glu	Ala	Val	Asn	Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala	
	290					295					300					
Leu	Lys	Ser	Tyr	Glu	Glu	Glu	Leu	Ala	Lys	Asp	Pro	Arg	Ile	Ala	Ala	
305					310					315					320	
Thr	Met	Glu	Asn	Ala	Gln	Lys	Gly	Glu	Ile	Met	Pro	Asn	Ile	Pro	Gln	
				325					330					335		
Met	Ser	Ala	Phe	Trp	Tyr	Ala	Val	Arg	Thr	Ala	Val	Ile	Asn	Ala	Ala	
			340					345				350				
Ser	Gly	Arg	Gln	Thr	Val	Asp	Glu	Ala	Leu	Lys	Asp	Ala	Gln	Thr	Asn	
		355					360					365				
Ser	Ser	Ser	His	His	His	His	His	His	Ala	Asn	Ser	Val	Pro	Leu	Val	
	370					375					380					
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<210> 38  
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<400> 38  
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<213> Artificial Sequence

<223> Oligonucleotide primer ZC40784

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24

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<400> 43  
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24

<210> 44  
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<400> 44  
 gggcattgcc aggacagctc ttttg

25

<210> 45  
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 cacctgccgc ccaggggcct tgcggcgggc ggcggggacc ccagggaccg aaggccatag 60  
 cggccggccc ctaggatccg aattctagaa gctttgtgtc tcaaaatctc tgatgttaca 120  
 t 121

<210> 46  
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<223> reverse zcytor19 knockout oligonucleotide

<400> 46

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gccggcgcgcg ctaggaattc tctagaggat ccaagctttt agaaaaactc atcgagcatc	120
aatg	125

<210> 47

<211> 22

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<400> 47

cctccttcca gaatgccacc tc	22
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<210> 48

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<210> 49

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<400> 49

ggaagataat gaaaggaaac cc	22
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<210> 50

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095898-11201



<213> Artificial Sequence

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21

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